

SEQUENCE LISTING

<110> Coleman, Timothy A. et al.

<120> Human Glycosylation Enzymes

<130> PF505D1

<150> PCT/US00/05325

<151> 2000-03-01

<150> 09/516,143

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<150> 60/122,409

<151> 1999-03-02

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<170> PatentIn Ver. 2.1

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Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg
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Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu

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210	215	220	

Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr
 225 230 235 240
 Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro
 245 250 255
 Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala
 260 265 270
 Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn
 275 280 285
 Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly
 290 295 300
 Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys
 305 310 315 320
 Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu
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 Met Ala Phe Pro Lys Lys Leu Gln Gly Leu Val Ala Ala Thr Ile
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 acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag 96
 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
 20 25 30
 tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg 144
 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
 35 40 45
 aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc 192
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
 50 55 60
 cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag 240
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
 65 70 75 80
 gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg 288
 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu

85	90	95			
gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala	100	105	110	336	
ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu	115	120	125	384	
aag gaa gtg gct gct gcc gcc cct gcc ctg cca ttt tat tac tat cac Lys Glu Val Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His	130	135	140	432	
att cct gcc ttg aca ggg gta aag att cgt gct gag gag ttg ttg gat Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp	145	150	155	160	480
ggg att ctg gat aag atc ccc acc ttc caa ggg ctg aaa ttc agt gat Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp	165	170	175		528
aca gat ctc tta gac ttc ggg caa tgt gtt gat cag aat cgc cag caa Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln	180	185	190		576
cag ttt gct ttc ctt ttt ggg gtg gat gag caa ctg ttg agt gct ctg Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu	195	200	205		624
gtg atg gga gca act gga gca gtg ggc agt ttt gta tcc aga gat tta Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu	210	215	220		672
tca act ttg ttg tca aac taggtttgg agtgtcacag accaaagcca Ser Thr Leu Leu Ser Asn	225	230			720
tcatgactct ggtctctggg attccaatgg gcccaccccg gcttccactg cagaaagcct ccagggagtt tactgatagt gctgaagcta aactgaagag cctggatttc ctttctttca					780
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Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
35 40 45

Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
50 55 60

Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
65 70 75 80

Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
85 90 95

Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
100 105 110

Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
115 120 125

Lys Glu Val Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His
130 135 140

Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
145 150 155 160

Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
165 170 175

Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
180 185 190

Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
195 200 205

Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu
210 215 220

Ser Thr Leu Leu Ser Asn
225 230